

Amendments to the Specification:

On Page 6, please delete the paragraph from lines 7-8 and replace it with the following replacement paragraph:

Figure 8 illustrates the ruler shown in ~~Figure 22A~~ Figure 7 after exposure to wound fluid that contained proteins from a microorganism specific to the sensors.

On Page 11, please delete the paragraph at lines 24 to 31 and replace it with the following replacement paragraph:

In another embodiment, the percent identity between two amino acid sequences can be determined by using the GAP program in the GCG software package (available from Accelrys, Inc. of San Diego, Calif., at ~~http://www.accelrys.com~~ www.accelrys.com, as of Aug. 31, 2001) using either a Blossom 63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be determined using a gap weight of 50 and a length weight of 3. Other preferred sequence comparison methods are described herein.

On Page 47, at line 31, please delete the CPI3 peptide listed there and replace it with the following replacement peptide:

CPI3 [Ac]-CGAMFLEAIPMSIPAAHHHHH-[OH] (SEQ ID NO: 23).